



OPEN ACCESS

EDITED BY

Jennifer Lovejoy,
Institute for Systems Biology (ISB),
United States

REVIEWED BY

Georgy Kurakin,
Independent Researcher, Tver', Russia

*CORRESPONDENCE

Mohamed Helmy,
✉ mohamed.helmy@usask.ca
Kumar Selvarajoo,
✉ Kumar_selvarajoo@a-star.edu.sg

RECEIVED 26 February 2026

REVISED 11 March 2026

ACCEPTED 13 March 2026

PUBLISHED 24 March 2026

CITATION

Helmy M and Selvarajoo K (2026) Systems
biology in the era of AI: "winter" or
"evolution"?

Front. Syst. Biol. 6:1818525.

doi: 10.3389/fsysb.2026.1818525

COPYRIGHT

© 2026 Helmy and Selvarajoo. This is an
open-access article distributed under the
terms of the [Creative Commons
Attribution License \(CC BY\)](#). The use,
distribution or reproduction in other
forums is permitted, provided the original
author(s) and the copyright owner(s) are
credited and that the original publication
in this journal is cited, in accordance with
accepted academic practice. No use,
distribution or reproduction is permitted
which does not comply with these terms.

Systems biology in the era of AI: "winter" or "evolution"?

Mohamed Helmy^{1,2,3,4,5,6*} and Kumar Selvarajoo^{6,7,8,9*}

¹Vaccine and Infectious Diseases Organization (VIDO), University of Saskatchewan, Saskatoon, SK, Canada, ²Vaccinology and Immunotherapeutics Program, School of Public Health, University of Saskatchewan, Saskatoon, SK, Canada, ³Department of Computer Science, University of Saskatchewan, Saskatoon, SK, Canada, ⁴Department of Biochemistry, Microbiology and Immunology, College of Medicine, University of Saskatchewan, Saskatoon, SK, Canada, ⁵Department of Computer Science, Idaho State University, Pocatello, ID, United States, ⁶Bioinformatics Institute (BII), Agency for Science, Technology and Research (A*STAR), Singapore, Singapore, ⁷Synthetic Biology Translational Research Program, Yong Loo Lin School of Medicine, National University of Singapore (NUS), Singapore, Singapore, ⁸Synthetic Biology for Clinical and Technological Innovation (SynCTI), National University of Singapore (NUS), Singapore, Singapore, ⁹School of Biological Sciences, Nanyang Technological University (NTU), Singapore, Singapore

KEYWORDS

artificial intelligence - AI, bioinformatics, data science, modelling, systems biology

Introduction

The sequencing and release of the draft human genome in June 2000 generated immense excitement, with expectations of a "quantum leap" in understanding molecular biology and human disease (Lander et al., 2001). Around the same period, *systems biology* emerged as a multidisciplinary effort uniting physics, mathematics, bioinformatics, and computational modeling. The field promised transformative advances in deciphering complex biological systems, their emergent behaviors, and potential therapeutic targets (Hasty et al., 2001; Kitano, 2002). This optimism spurred the launch of dedicated journals such as *Molecular Systems Biology* (EMBO), *BMC Systems Biology*, *PLOS Computational Biology*, and *npj Systems Biology and Applications*.

Systems biology indeed enabled discoveries unattainable through reductionist approaches alone. For example, dynamic models of inflammatory responses offered mechanistic insights and identified regulators that were later experimentally validated (Hayashi et al., 2013; Caldwell et al., 2014). Its core strength lies in moving from descriptive correlations to causal explanations, incorporating nonlinearity, feedback, and emergent properties (Kitano, 2001).

Yet despite its promise, the field has faced hurdles. Building dynamic or kinetic models of biological networks, intended to predict changes in molecular concentrations over time, has proven slow. The difficulty stems from quantifying large numbers of model parameters, limited availability of time-resolved data, and the heavy mathematical demands of parameter estimation and optimization.

As with stem cell biology and gene therapy, systems biology has undergone recalibration: early enthusiasm outpaced translation, and breakthroughs in curing major diseases such as cancer and diabetes remain elusive (Daley, 2012; Kaemmerer, 2018). Progress now depends on new technologies, particularly automated and scalable modeling approaches.

The rise of AI in biomedicine

In recent years, artificial intelligence (AI), especially generative models, has been widely adopted to analyze multi-omics datasets, generate artificial data, and even build *in silico* cancer genomes (Heydari et al., 2022; Díaz-Navarro et al., 2025; Woerner et al., 2025). AI

excels at uncovering hidden patterns in vast datasets, often at scales far beyond human capacity. However, these models remain largely predictive “black boxes,” powerful for classification and pattern recognition but offering little mechanistic explanation (Helmy et al., 2020).

Enthusiasm has nonetheless soared. Global investment in AI-driven biomedical research has increased dramatically (Chibambo, 2025; Clarke, 2025; Greenacre, 2025; MDDI, 2025; NIH, 2025). This raises a philosophical question: should biomedicine prioritize rapid prediction without explanation, or aim for explanations that enable reliable, reproducible prediction?

Is systems biology facing a winter?

Foundational systems biology research now faces critical challenges. The closure of *BMC Systems Biology* in 2019, together with declining impact factors of related journals, points to reduced visibility and engagement in the field. Although impact factor is an imperfect metric, it reflects average citation activity and is therefore a reasonable proxy for community interest in this context, especially when contrasted with the rapid rise of AI-focused outlets such as *npj Digital Medicine* and *The Lancet Digital Health* (Figure 1). This shift reflects a redistribution of attention and resources. Yet such rapid swings risk undervaluing the mechanistic insights systems biology uniquely provides. If training pipelines focus too heavily on AI, future scientists may excel at algorithmic manipulation but lack the ability to design or test mechanistic hypotheses, skills that, once lost, are slow to rebuild (Pellegrina and Helmy, 2025).

Are we witnessing the first “systems biology winter,” akin to the AI winters where unmet expectations deflated momentum (Toosi et al., 2021)? Or is this a natural stage of maturation? As shown in Figure 1, based on journal impact, systems biology appears to have plateaued or gradually declining, while AI is experiencing exponential growth.

Integration rather than competition

A more constructive interpretation is that systems biology is evolving into a complementary partner to AI. Rather than competing, the two can be integrated.

Systems biology provides mechanistic guardrails, ensuring AI predictions remain biologically plausible. AI, in turn, accelerates discovery by scanning high-dimensional datasets for candidate interactions (Helmy et al., 2020; Yeo and Selvarajoo, 2022). This synergy aligns with the vision of *Digital Twins*, virtual representations of patients that combine mechanistic physiology with AI-driven personalization to predict disease trajectories and treatment responses (Laubenbacher et al., 2022; Helmy et al., 2024).

Recent advances in deep learning for causal network inference (Lagemann et al., 2023; Van Hilten et al., 2024) highlight both promise and limitations: predictions are largely static and often inaccurate (Ahlmann-Eltze et al., 2025). Embedding systems biology models within AI frameworks could provide the missing temporal and mechanistic structure.

Integration also addresses ethical imperatives. Black-box predictions in medicine risk misleading clinical practice and policy if not grounded in mechanistic understanding (Budhkar et al., 2025). As argued in emerging frameworks for responsible AI (Helmy et al., 2025), interpretability and reproducibility are ethical requirements, not optional features.

A roadmap for the future

To accelerate integration, we propose a staged roadmap:

- Short-term (0–3 years):
 - Embed dynamic systems models into AI workflows for temporal plausibility.

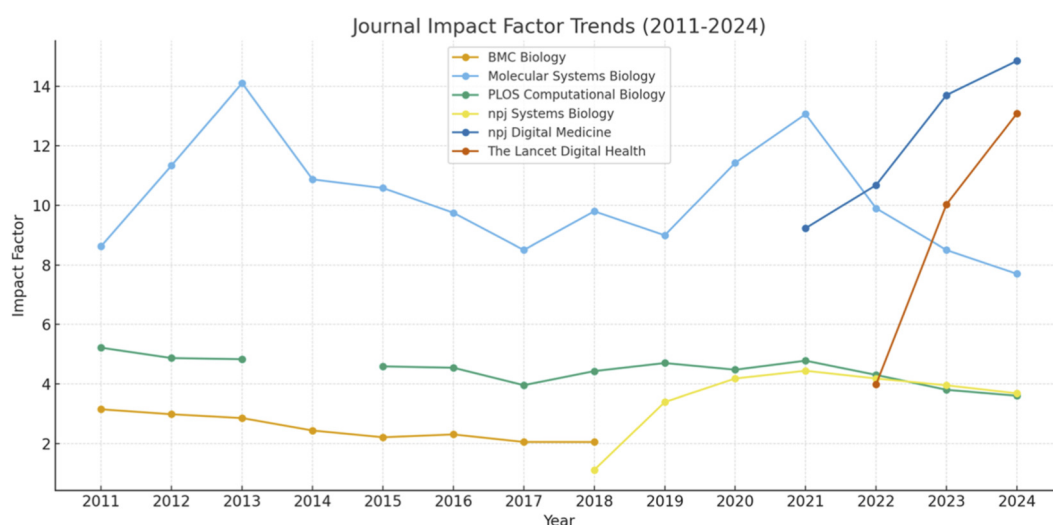


FIGURE 1

The impact factor of Systems Biology and Biomedical AI journals since 2011 (retrieved from journal websites and Web of Science). Gradual decline in BMC Systems Biology (ceased in 2019) and PLOS Computational Biology, whereas a surge in npj Digital Medicine and The Lancet Digital Medicine.

- Establish benchmarking standards where AI predictions are cross-validated with mechanistic models.
- Mid-term (3–7 years):
 - Funding agencies and journals prioritize integrative projects.
 - Develop collaborative platforms linking systems biology datasets with AI pipelines.
- Long-term (7+ years):
 - Redesign training programs to blend algorithmic literacy with mechanistic reasoning.
 - Foster translational pipelines where AI-driven discoveries are grounded in systems biology for clinical application.

Conclusion

While systems biology no longer commands the excitement of the early 2000s, it remains indispensable. Its focus on causality, feedback, and emergent properties ensures biomedical discoveries are mechanistically grounded and reproducible. AI, by contrast, provides unprecedented predictive power but risks fragility without biological grounding. The future lies in integration. By combining AI's scale and speed with systems biology's explanatory depth, the biomedical sciences can achieve robust prediction and understanding. Whether systems biology faces a "winter" or an evolutionary transformation will depend on whether the community embraces this hybrid vision. With thoughtful policy, training, and interdisciplinary collaboration, systems biology can rise again, not as AI's competitor, but as its essential partner.

Author contributions

MH: Data curation, Formal Analysis, Validation, Writing – original draft, Writing – review and editing. KS: Conceptualization, Data curation, Formal Analysis, Methodology, Supervision, Visualization, Writing – original draft, Writing – review and editing.

Funding

The author(s) declared that financial support was received for this work and/or its publication. This work was supported by the core research fund of ASTAR Bioinformatics Institute (KS), and the Vaccine and Infectious Disease Organization (VIDO), University of Saskatchewan (MH).

References

- Ahlmann-Eltze, C., Huber, W., and Anders, S. (2025). Deep-learning-based gene perturbation effect prediction does not yet outperform simple linear baselines. *Nat. Methods* 22, 1657–1661. doi:10.1038/S41592-025-02772-6
- Budhkar, A., Song, Q., Su, J., and Zhang, X. (2025). Demystifying the black box: a survey on explainable artificial intelligence (XAI) in bioinformatics. *Comput. Struct. Biotechnol. J.* 27, 346–359. doi:10.1016/J.CSB.2024.12.027
- Caldwell, A. B., Birnbaum, H. A., Cheng, Z., Hoffmann, A., and Vargas, J. D. (2014). Network dynamics determine the autocrine and paracrine signaling functions of TNF. *Genes Dev.* 28, 2120–2133. doi:10.1101/GAD.244749.114
- Chibambo, R. (2025). Canada launches \$200M genomics data initiative to drive precision health and economic growth - GenomeCanada. Available online at: <https://genomecanada.ca/canada-launches-200m-genomics-data-initiative-to-drive-precision-health-and-economic-growth/> (Accessed August 25, 2025).
- Clarcke, O. (2025). Government to invest over £2 billion in the UK's AI ecosystem | Osborne Clarke. Available online at: <https://www.osborneclarke.com/insights/>

Acknowledgment

VIDO receives operational funding from the Government of Saskatchewan through Innovation Saskatchewan and the Ministry of Agriculture and from the Canada Foundation for Innovation through the Major Science Initiatives Fund. Published as VIDO manuscript series no. 1131.

Conflict of interest

The author(s) declared that this work was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

The author MH declared that they were an editorial board member of Frontiers at the time of submission. This had no impact on the peer review process and the final decision.

Generative AI statement

The author(s) declared that generative AI was used in the creation of this manuscript. The author(s) verify and take full responsibility for the use of generative AI in the preparation of this manuscript. Generative AI was used to assist with language refinement, structural organization, and editing of the text. It was also used to suggest improvements in clarity, coherence, and phrasing of specific sections. All scientific content, interpretations, arguments, and conclusions were developed, verified, and approved by the authors. No generative AI tools were used to generate data, results, or original scientific claims. The authors critically reviewed and validated all outputs to ensure accuracy, integrity, and compliance with ethical standards.

Any alternative text (alt text) provided alongside figures in this article has been generated by Frontiers with the support of artificial intelligence and reasonable efforts have been made to ensure accuracy, including review by the authors wherever possible. If you identify any issues, please contact us.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

- government-invest-over-ps2-billion-uks-ai-ecosystem (Accessed August 25, 2025).
- Daley, G. Q. (2012). The promise and perils of stem cell therapeutics. *Cell Stem Cell* 10, 740–749. doi:10.1016/j.stem.2012.05.010
- Díaz-Navarro, A., Zhang, X., Jiao, W., Wang, B., and Stein, L. (2025). *In silico* generation of synthetic cancer genomes using generative AI. *Cell Genomics* 2024, 100969. doi:10.1101/2024.10.17.618896
- Greenacre, M. (2025). EU to invest €50B to “supercharge” innovation in artificial intelligence | science|business. Available online at: <https://sciencebusiness.net/news/eu-budget/eu-invest-eu50b-supercharge-innovation-artificial-intelligence> (Accessed August 25, 2025).
- Hasty, J., McMillen, D., Isaacs, F., and Collins, J. J. (2001). Computational studies of gene regulatory networks: in numero molecular biology. *Nat. Rev. Genet.* 2, 268–279. doi:10.1038/35066056
- Hayashi, K., Piras, V., Tabata, S., Tomita, M., and Selvarajoo, K. (2013). A systems biology approach to suppress TNF-induced proinflammatory gene expressions. *Cell Commun. Signal.* 11, 1–15. doi:10.1186/1478-811X-11-84/FIGURES/5
- Helmy, M., Smith, D., and Selvarajoo, K. (2020). Systems biology approaches integrated with artificial intelligence for optimized metabolic engineering. *Metab. Eng. Commun.* 11, e00149. doi:10.1016/j.mec.2020.e00149
- Helmy, M., Elhalis, H., Rashid, M. M., and Selvarajoo, K. (2024). Can digital twin efforts shape microorganism-based alternative food? *Curr. Opin. Biotechnol.* 87, 103115. doi:10.1016/J.COPBIO.2024.103115
- Helmy, M., Jin, L., Alhossary, A., Mansour, T., Pellagrini, D., and Selvarajoo, K. (2025). Ten simple rules for optimal and careful use of generative AI in science. *PLoS Comput. Biol.* 21, e1013588. doi:10.1371/journal.pcbi.1013588
- Heydari, A. A., Davalos, O. A., Zhao, L., Hoyer, K. K., and Sindi, S. S. (2022). ACTIVA: realistic single-cell RNA-seq generation with automatic cell-type identification using introspective variational autoencoders. *Bioinformatics* 38, 2194–2201. doi:10.1093/BIOINFORMATICS/BTAC095
- Kaemmerer, W. F. (2018). How will the field of gene therapy survive its success? *Bioeng. Transl. Med.* 3, 166–177. doi:10.1002/BTM2.10090
- Kitano, H. (2001). *Foundations of systems biology*. USA: MIT press.
- Kitano, H. (2002). Systems biology: a brief overview. *Science* 295, 1662–1664. doi:10.1126/science.1069492
- Lagemann, K., Lagemann, C., Taschler, B., and Mukherjee, S. (2023). Deep learning of causal structures in high dimensions under data limitations. *Nat. Mach. Intell.* 5, 1306–1316. doi:10.1038/S42256-023-00744-Z
- Lander, E. S., Linton, L. M., Birren, B., Nusbaum, C., Zody, M. C., Baldwin, J., et al. (2001). Initial sequencing and analysis of the human genome. *Nat.* 2001 409 (6822), 860–921. doi:10.1038/35057062
- Laubenbacher, R., Niarakis, A., Helikar, T., An, G., Shapiro, B., Malik-Sheriff, R. S., et al. (2022). Building digital twins of the human immune system: toward a roadmap. *NPJ Digit. Med.* 5, 64. doi:10.1038/S41746-022-00610-Z
- MDDI (2025). Further S\$120M investment in “AI for Science” | Ministry of digital development and information of the Republic of Singapore. Available online at: <https://www.mddi.gov.sg/newsroom/further-120m-investment-in-ai-for-science> (Accessed August 25, 2025).
- NIH (2025). Bridge to artificial intelligence (Bridge2AI) | NIH common fund. Available online at: <https://commonfund.nih.gov/bridge2ai> (Accessed August 25, 2025).
- Pellegrina, D., and Helmy, M. (2025). AI for scientific integrity: detecting ethical breaches, errors, and misconduct in manuscripts. *Front. Artif. Intell.* 8, 1644098. doi:10.3389/FRAI.2025.1644098
- Toosi, A., Bottino, A. G., Saboury, B., Siegel, E., and Rahmim, A. (2021). A brief history of AI: how to prevent another winter (A critical review). *Pet. Clin.* 16, 449–469. doi:10.1016/j.cpet.2021.07.001
- Van Hilten, A., Katz, S., Saccenti, E., Niessen, W. J., and Roshchupkin, G. V. (2024). Designing interpretable deep learning applications for functional genomics: a quantitative analysis. *Brief. Bioinform.* 25, bbae449. doi:10.1093/BIB/BBAE449
- Woerner, J., Nam, Y., Jung, S. H., Shivakumar, M., Lee, M., Choe, E. K., et al. (2025). Leveraging automated machine learning to predict colon cancer prognosis from clinical features and risk groups: a retrospective cohort study. *Eur. J. Surg. Oncol.* 51, 110194. doi:10.1016/j.ejso.2025.110194
- Yeo, H. C., and Selvarajoo, K. (2022). Machine learning alternative to systems biology should not solely depend on data. *Brief. Bioinform.* 23, 1–6. doi:10.1093/bib/bbac436